10/530217

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SEQUENCE LISTING

<110>   ONCOTHERAPY SCIENCE, INC.

        JAPAN AS REPRESENTED BY THE PRESIDENT OF THE UNIVERSITY OF TOKYO

<120>   GENES AND POLYPEPTIDES RELATING TO HUMAN MYELOID LEUKEMIA

<130>   ONC-A0213P2

<150>   US 60/414,867

<151>   2002-09-30

<160>   16

<170>   PatentIn version 3.1

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ctgtgtgatg gacgtctg   18

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<223> Target sequence for Si-RNA

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gtacgtgcag caggagaac   19

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gaagcagcac gacttcttc   19

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                                                            Met Ser
                                                             1


gag gcc cgc agg gac agc acg agc agc ctg cag cgc aag aag cca ccc      164
Glu Ala Arg Arg Asp Ser Thr Ser Ser Leu Gln Arg Lys Lys Pro Pro
        5                   10                  15


tgg cta aag ctg gac att ccc tct gcg gtg ccc ctg acg gca gaa gag      212
Trp Leu Lys Leu Asp Ile Pro Ser Ala Val Pro Leu Thr Ala Glu Glu
    20                  25                  30
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ccc agc ttc ctg cag ccc ctg agg cga cag gct ttc ctg agg agt gtg 260
Pro Ser Phe Leu Gln Pro Leu Arg Arg Gln Ala Phe Leu Arg Ser Val
35   40   45   50

agt atg cca gcc gag aca gcc cac atc tct tca ccc cac cat gag ctc 308
Ser Met Pro Ala Glu Thr Ala His Ile Ser Ser Pro His His Glu Leu
    55   60   65

cgg cgg ccg gtg ctg caa cgc cag acg tcc atc aca cag acc atc cgc 356
Arg Arg Pro Val Leu Gln Arg Gln Thr Ser Ile Thr Gln Thr Ile Arg
    70   75   80

agg ggg acc gcc gac tgg ttt gga gtg agc aag gac agt gac agc acc 404
Arg Gly Thr Ala Asp Trp Phe Gly Val Ser Lys Asp Ser Asp Ser Thr
    85   90   95

cag aaa tgg cag cgc aag agc atc cgt cac tgc agc cag cgc tac ggg 452
Gln Lys Trp Gln Arg Lys Ser Ile Arg His Cys Ser Gln Arg Tyr Gly
    100   105   110

aag ctg aag ccc cag gtc ctc cgg gag ctg gac ctg ccc agc cag gac 500
Lys Leu Lys Pro Gln Val Leu Arg Glu Leu Asp Leu Pro Ser Gln Asp
115   120   125   130

aac gtg tcg ctg acc agc acc gag acg cca ccc cca ctc tac gtg ggg 548

Asn Val Ser Leu Thr Ser Thr Glu Thr Pro Pro Pro Leu Tyr Val Gly
            135   140   145

cca tgc cag ctg ggc atg cag aag atc ata gac ccc ctg gcc cgt ggc   596
Pro Cys Gln Leu Gly Met Gln Lys Ile Ile Asp Pro Leu Ala Arg Gly
            150   155   160

cgt gcc ttc cgt gtg gca gat gac act gcg gaa ggc ctg agt gcc cca   644
Arg Ala Phe Arg Val Ala Asp Asp Thr Ala Glu Gly Leu Ser Ala Pro
            165   170   175

cac act ccc gtc acg ccg ggt gct gcc tcc ctc tgc tcc ttc tcc agc   692
His Thr Pro Val Thr Pro Gly Ala Ala Ser Leu Cys Ser Phe Ser Ser
            180   185   190

tcc cgc tca ggt ttc cac cgg ctc ccg cgg cgg cgc aag cga gag tcg   740
Ser Arg Ser Gly Phe His Arg Leu Pro Arg Arg Arg Lys Arg Glu Ser
    195   200   205   210

gtg gcc aag atg agc ttc cgg gcg gcc gca gcg ctg atg aaa ggc cgc   788
Val Ala Lys Met Ser Phe Arg Ala Ala Ala Ala Leu Met Lys Gly Arg
            215   220   225

tcc gtt agg gat ggc acc ttt cgc cgg gca cgg cgt cga agc ttc act   836
Ser Val Arg Asp Gly Thr Phe Arg Arg Ala Arg Arg Arg Ser Phe Thr
            230   235   240

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cca gct agc ttt ctg gag gag gac aca act gat ttc ccc gat gag ctg      884
Pro Ala Ser Phe Leu Glu Glu Asp Thr Thr Asp Phe Pro Asp Glu Leu
         245             250             255


gac aca tcc ttc ttt gcc cgg gaa ggt atc ctc cat gaa gag ctg tcc      932
Asp Thr Ser Phe Phe Ala Arg Glu Gly Ile Leu His Glu Glu Leu Ser
     260             265             270


aca tac ccg gat gaa gtt ttc gag tcc cca tcg gag gca gcg cta aag      980
Thr Tyr Pro Asp Glu Val Phe Glu Ser Pro Ser Glu Ala Ala Leu Lys
275             280             285             290


gac tgg gag aag gca ccg gag cag gcg gac ctc acc ggc ggg gcc ctg     1028
Asp Trp Glu Lys Ala Pro Glu Gln Ala Asp Leu Thr Gly Gly Ala Leu
         295             300             305


gac cgc agc gag ctt gag cgc agc cac ctg atg ctg ccc ttg gag cga     1076
Asp Arg Ser Glu Leu Glu Arg Ser His Leu Met Leu Pro Leu Glu Arg
         310             315             320


ggc tgg cgg aag cag aag gag ggc gcc gca gcc ccg cag ccc aag gtg     1124
Gly Trp Arg Lys Gln Lys Glu Gly Ala Ala Ala Pro Gln Pro Lys Val
         325             330             335


cgg ctc cga cag gag gtg gtg agc acc gcg ggg ccg cga cgg ggc cag     1172
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Arg Leu Arg Gln Glu Val Val Ser Thr Ala Gly Pro Arg Arg Gly Gln

    340   345   350

cgt atc gcg gtg ccg gtg cgc aag ctc ttc gcc cgg gag aag cgg ccg   1220

Arg Ile Ala Val Pro Val Arg Lys Leu Phe Ala Arg Glu Lys Arg Pro

355   360   365   370

tat ggg ctg ggc atg gtg gga cgg ctc acc aac cgc acc tac cgc aag   1268

Tyr Gly Leu Gly Met Val Gly Arg Leu Thr Asn Arg Thr Tyr Arg Lys

    375   380   385

cgc atc gac agc ttc gtc aag cgc cag atc gag gac atg gac gac cac   1316

Arg Ile Asp Ser Phe Val Lys Arg Gln Ile Glu Asp Met Asp Asp His

    390   395   400

agg ccc ttc ttc acc tac tgg ctt acc ttc gtg cac tcg ctc gtc acc   1364

Arg Pro Phe Phe Thr Tyr Trp Leu Thr Phe Val His Ser Leu Val Thr

    405   410   415

atc cta gcc gtg tgc atc tat ggc atc gcg ccc gtg ggc ttc tcg cag   1412

Ile Leu Ala Val Cys Ile Tyr Gly Ile Ala Pro Val Gly Phe Ser Gln

    420   425   430

cat gag acg gtg gac tcg gtg ctg cgg aac cgc ggg gtc tac gag aac   1460

His Glu Thr Val Asp Ser Val Leu Arg Asn Arg Gly Val Tyr Glu Asn

435   440   445   450

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gtc aag tac gtg cag cag gag aac ttc tgg atc ggg ccc agc tcg gag          1508
Val Lys Tyr Val Gln Gln Glu Asn Phe Trp Ile Gly Pro Ser Ser Glu
        455                 460                 465


gcc ctc atc cac ctg ggc gcc aag ttt tcg ccc tgc atg cgc cag gac          1556
Ala Leu Ile His Leu Gly Ala Lys Phe Ser Pro Cys Met Arg Gln Asp
        470                 475                 480


ccg cag gtg cac agc ttc att cgc tcg gcg cgc gag cgc gag aag cac          1604
Pro Gln Val His Ser Phe Ile Arg Ser Ala Arg Glu Arg Glu Lys His
        485                 490                 495


tcc gcc tgc tgc gtg cgc aac gac agg tcg ggc tgc gtg cag acc tcg          1652
Ser Ala Cys Cys Val Arg Asn Asp Arg Ser Gly Cys Val Gln Thr Ser
        500                 505                 510


gag gag gag tgc tcg tcc acg ctg gca gtg tgg gtg aag tgg ccc atc          1700
Glu Glu Glu Cys Ser Ser Thr Leu Ala Val Trp Val Lys Trp Pro Ile
    515             520             525                 530


cat ccc agc gcc cca gag ctt gcg ggc cac aag aga cag ttt ggc tct          1748
His Pro Ser Ala Pro Glu Leu Ala Gly His Lys Arg Gln Phe Gly Ser
            535                 540                 545


gtc tgc cac cag gat ccc agg gtg tgt gat gag ccc tcc tcc gaa gac          1796
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Val Cys His Gln Asp Pro Arg Val Cys Asp Glu Pro Ser Ser Glu Asp
        550                 555                 560


cct cat gag tgg cca gaa gac atc acc aag tgg ccg atc tgc acc aaa          1844
Pro His Glu Trp Pro Glu Asp Ile Thr Lys Trp Pro Ile Cys Thr Lys
        565                 570                 575


aac agc gct ggg aac cac acc aac cat ccc cac atg gac tgt gtc atc          1892
Asn Ser Ala Gly Asn His Thr Asn His Pro His Met Asp Cys Val Ile
        580                 585                 590


aca gga cgg ccc tgc tgc att ggc acc aag ggc agg tgt gag atc acc          1940
Thr Gly Arg Pro Cys Cys Ile Gly Thr Lys Gly Arg Cys Glu Ile Thr
595                 600                 605                 610


tcc cgg gag tac tgt gac ttc atg agg ggc tac ttc cat gag gag gcc          1988
Ser Arg Glu Tyr Cys Asp Phe Met Arg Gly Tyr Phe His Glu Glu Ala
        615                 620                 625


acg ctc tgc tct cag gtg cac tgc atg gat gat gtg tgt ggg ctc ctg          2036
Thr Leu Cys Ser Gln Val His Cys Met Asp Asp Val Cys Gly Leu Leu
        630                 635                 640


cct ttt ctc aac ccc gag gtg cct gac cag ttc tac cgc ctg tgg cta          2084
Pro Phe Leu Asn Pro Glu Val Pro Asp Gln Phe Tyr Arg Leu Trp Leu
        645                 650                 655
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tcc ctc ttc ctg cac gcc ggg atc ttg cac tgc ctg gtg tcc atc tgc        2132
Ser Leu Phe Leu His Ala Gly Ile Leu His Cys Leu Val Ser Ile Cys
    660             665                 670


ttc cag atg act gtc ctg cgg gac ctg gag aag ctg gca ggc tgg cac        2180
Phe Gln Met Thr Val Leu Arg Asp Leu Glu Lys Leu Ala Gly Trp His
675             680                 685                 690


cgc ata gcc atc atc tac ctg ctg agt ggt gtc acc ggc aac ctg gcc        2228
Arg Ile Ala Ile Ile Tyr Leu Leu Ser Gly Val Thr Gly Asn Leu Ala
                695                 700                 705


agt gcc atc ttc ctg cca tac cga gca gag gtg ggt cct gct ggc tcc        2276
Ser Ala Ile Phe Leu Pro Tyr Arg Ala Glu Val Gly Pro Ala Gly Ser
        710                 715                 720


cag ttc ggc atc ctg gcc tgc ctc ttc gtg gag ctc ttc cag agc tgg        2324
Gln Phe Gly Ile Leu Ala Cys Leu Phe Val Glu Leu Phe Gln Ser Trp
        725                 730                 735


cag atc ctg gcg cgg ccc tgg cgt gcc ttc ttc aag ctg ctg gct gtg        2372
Gln Ile Leu Ala Arg Pro Trp Arg Ala Phe Phe Lys Leu Leu Ala Val
    740                 745                 750


gtg ctc ttc ctc ttc acc ttt ggg ctg ctg ccg tgg att gac aac ttt        2420
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Val Leu Phe Leu Phe Thr Phe Gly Leu Leu Pro Trp Ile Asp Asn Phe

755   760   765   770

gcc cac atc tcg ggg ttc atc agt ggc ctc ttc ctc tcc ttc gcc ttc   2468

Ala His Ile Ser Gly Phe Ile Ser Gly Leu Phe Leu Ser Phe Ala Phe

                        775   780   785

ttg ccc tac atc agc ttt ggc aag ttc gac ctg tac cgg aaa cgc tgc   2516

Leu Pro Tyr Ile Ser Phe Gly Lys Phe Asp Leu Tyr Arg Lys Arg Cys

            790   795   800

cag atc atc atc ttt cag gtg gtc ttc ctg ggc ctc ctg gct ggc ctg   2564

Gln Ile Ile Ile Phe Gln Val Val Phe Leu Gly Leu Leu Ala Gly Leu

            805   810   815

gtg gtc ctc ttc tac gtc tat cct gtc cgc tgt gag tgg tgt gag ttc   2612

Val Val Leu Phe Tyr Val Tyr Pro Val Arg Cys Glu Trp Cys Glu Phe

            820   825   830

ctc acc tgc atc ccc ttc act gac aag ttc tgt gag aag tac gaa ctg   2660

Leu Thr Cys Ile Pro Phe Thr Asp Lys Phe Cys Glu Lys Tyr Glu Leu

835   840   845   850

gac gct cag ctc cac tga gctggctgcg ggctccagcg gccgtgtgct   2708

Asp Ala Gln Leu His

                855

ccagcaggcc agagccagac acgacctccc tgagcctcac aggcttacag gagtcacctg   2768

ctccatgtgg ggactggcct gtttcctgaa cacagacctc tttcttgtgc cttgttcact   2828

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<212> PRT

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                20   25   30

Glu Glu Pro Ser Phe Leu Gln Pro Leu Arg Arg Gln Ala Phe Leu Arg
            35   40   45

Ser Val Ser Met Pro Ala Glu Thr Ala His Ile Ser Ser Pro His His

    50   55   60

Glu Leu Arg Arg Pro Val Leu Gln Arg Gln Thr Ser Ile Thr Gln Thr

65   70   75   80

Ile Arg Arg Gly Thr Ala Asp Trp Phe Gly Val Ser Lys Asp Ser Asp

            85   90   95

Ser Thr Gln Lys Trp Gln Arg Lys Ser Ile Arg His Cys Ser Gln Arg

            100   105   110

Tyr Gly Lys Leu Lys Pro Gln Val Leu Arg Glu Leu Asp Leu Pro Ser

        115   120   125

Gln Asp Asn Val Ser Leu Thr Ser Thr Glu Thr Pro Pro Pro Leu Tyr

    130   135   140

Val Gly Pro Cys Gln Leu Gly Met Gln Lys Ile Ile Asp Pro Leu Ala

145   150   155   160

Arg Gly Arg Ala Phe Arg Val Ala Asp Asp Thr Ala Glu Gly Leu Ser

            165   170   175

Ala Pro His Thr Pro Val Thr Pro Gly Ala Ala Ser Leu Cys Ser Phe

              180   185   190

Ser Ser Ser Arg Ser Gly Phe His Arg Leu Pro Arg Arg Arg Lys Arg
              195   200   205

Glu Ser Val Ala Lys Met Ser Phe Arg Ala Ala Ala Ala Leu Met Lys
              210   215   220

Gly Arg Ser Val Arg Asp Gly Thr Phe Arg Arg Ala Arg Arg Arg Ser
225   230   235   240

Phe Thr Pro Ala Ser Phe Leu Glu Glu Asp Thr Thr Asp Phe Pro Asp
                       245   250   255

Glu Leu Asp Thr Ser Phe Phe Ala Arg Glu Gly Ile Leu His Glu Glu
                       260   265   270

Leu Ser Thr Tyr Pro Asp Glu Val Phe Glu Ser Pro Ser Glu Ala Ala
                       275   280   285

Leu Lys Asp Trp Glu Lys Ala Pro Glu Gln Ala Asp Leu Thr Gly Gly
              290   295   300

Ala Leu Asp Arg Ser Glu Leu Glu Arg Ser His Leu Met Leu Pro Leu
305   310   315   320

Glu Arg Gly Trp Arg Lys Gln Lys Glu Gly Ala Ala Ala Pro Gln Pro
          325   330   335

Lys Val Arg Leu Arg Gln Glu Val Val Ser Thr Ala Gly Pro Arg Arg
          340   345   350

Gly Gln Arg Ile Ala Val Pro Val Arg Lys Leu Phe Ala Arg Glu Lys
          355   360   365

Arg Pro Tyr Gly Leu Gly Met Val Gly Arg Leu Thr Asn Arg Thr Tyr
          370   375   380

Arg Lys Arg Ile Asp Ser Phe Val Lys Arg Gln Ile Glu Asp Met Asp
385   390   395   400

Asp His Arg Pro Phe Phe Thr Tyr Trp Leu Thr Phe Val His Ser Leu
          405   410   415

Val Thr Ile Leu Ala Val Cys Ile Tyr Gly Ile Ala Pro Val Gly Phe
          420   425   430

Ser Gln His Glu Thr Val Asp Ser Val Leu Arg Asn Arg Gly Val Tyr
          435   440   445

Glu Asn Val Lys Tyr Val Gln Gln Glu Asn Phe Trp Ile Gly Pro Ser
          450   455   460

Ser Glu Ala Leu Ile His Leu Gly Ala Lys Phe Ser Pro Cys Met Arg
465   470   475   480

Gln Asp Pro Gln Val His Ser Phe Ile Arg Ser Ala Arg Glu Arg Glu
                485   490   495

Lys His Ser Ala Cys Cys Val Arg Asn Asp Arg Ser Gly Cys Val Gln
                500   505   510

Thr Ser Glu Glu Glu Cys Ser Ser Thr Leu Ala Val Trp Val Lys Trp
        515   520   525

Pro Ile His Pro Ser Ala Pro Glu Leu Ala Gly His Lys Arg Gln Phe
        530   535   540

Gly Ser Val Cys His Gln Asp Pro Arg Val Cys Asp Glu Pro Ser Ser
545   550   555   560

Glu Asp Pro His Glu Trp Pro Glu Asp Ile Thr Lys Trp Pro Ile Cys
                565   570   575

Thr Lys Asn Ser Ala Gly Asn His Thr Asn His Pro His Met Asp Cys
        580   585   590

Val Ile Thr Gly Arg Pro Cys Cys Ile Gly Thr Lys Gly Arg Cys Glu

    595   600   605

Ile Thr Ser Arg Glu Tyr Cys Asp Phe Met Arg Gly Tyr Phe His Glu
  610   615   620

Glu Ala Thr Leu Cys Ser Gln Val His Cys Met Asp Asp Val Cys Gly
625   630   635   640

Leu Leu Pro Phe Leu Asn Pro Glu Val Pro Asp Gln Phe Tyr Arg Leu
    645   650   655

Trp Leu Ser Leu Phe Leu His Ala Gly Ile Leu His Cys Leu Val Ser
    660   665   670

Ile Cys Phe Gln Met Thr Val Leu Arg Asp Leu Glu Lys Leu Ala Gly
    675   680   685

Trp His Arg Ile Ala Ile Ile Tyr Leu Leu Ser Gly Val Thr Gly Asn
  690   695   700

Leu Ala Ser Ala Ile Phe Leu Pro Tyr Arg Ala Glu Val Gly Pro Ala
705   710   715   720

Gly Ser Gln Phe Gly Ile Leu Ala Cys Leu Phe Val Glu Leu Phe Gln
    725   730   735

Ser Trp Gln Ile Leu Ala Arg Pro Trp Arg Ala Phe Phe Lys Leu Leu
        740   745   750

Ala Val Val Leu Phe Leu Phe Thr Phe Gly Leu Leu Pro Trp Ile Asp
        755   760   765

Asn Phe Ala His Ile Ser Gly Phe Ile Ser Gly Leu Phe Leu Ser Phe
        770   775   780

Ala Phe Leu Pro Tyr Ile Ser Phe Gly Lys Phe Asp Leu Tyr Arg Lys
785   790   795   800

Arg Cys Gln Ile Ile Ile Phe Gln Val Val Phe Leu Gly Leu Leu Ala
                805   810   815

Gly Leu Val Val Leu Phe Tyr Val Tyr Pro Val Arg Cys Glu Trp Cys
                820   825   830

Glu Phe Leu Thr Cys Ile Pro Phe Thr Asp Lys Phe Cys Glu Lys Tyr
        835   840   845

Glu Leu Asp Ala Gln Leu His
        850   855